



SEQUENCE LISTING

110 Pryggvason, Karl
Salo, Sirpa

<120> Use of antibodies to the gamma 2 chain of laminin 5 to inhibit tumor growth and metastasis

<130> 02-1147

<150> 60/422,009

<151> 2002-10-29

<150> US 09/756,071

<151> 2001-01-08

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 5200

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118)..(3699)

<223>

<220>

<221> sig_peptide

<222> (118)..(183)

<223>

<400> 1

gaccacctga tcgaaggaaa aggaaggcac agcggagcgc agagtgagaa ccaccaaccg 60

aggcgccggg cagcgacccc tgcagcggag acagagactg agcggcccg 117

atg cct gcg ctc tgg ctg ggc tgc tgc ctc tgc ttc tgc ctc ctc ctg 165

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu 1 5 10 15

ccc gca gcc cg 213
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly 20 25 30

aag tcc agg cag tgt atc ttt gat cgg gaa ctt cac aga caa act ggt 261
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly 35 40 45

aat gga ttc cgc tgc ctc aac tgc aat gac aac act gat ggc att cac 309
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His 50 55 60

tgc gag aag tgc aag aat ggc ttt tac cgg cac aga gaa agg gac cgc 357

Cys	Glu	Lys	Cys	Lys	Asn	Gly	Phe	Tyr	Arg	His	Arg	Glu	Arg	Asp	Arg	
65					70					75				80		
tgt	ttg	ccc	tgc	aat	tgt	aac	tcc	aaa	ggt	tct	ctt	agt	gct	cga	tgt	405
Cys	Leu	Pro	Cys	Asn	Cys	Asn	Ser	Lys	Gly	Ser	Leu	Ser	Ala	Arg	Cys	
					85					90				95		
gac	aac	tct	gga	cgg	tgc	agc	tgt	aaa	cca	ggg	gtg	aca	gga	gcc	aga	453
Asp	Asn	Ser	Gly	Arg	Cys	Ser	Cys		Lys	Pro	Gly	Val	Thr	Gly	Ala	Arg
					100					105				110		
tgc	gac	cga	tgt	ctg	cca	ggc	ttc	cac	atg	ctc	acg	gat	gcg	ggg	tgc	501
Cys	Asp	Arg	Cys	Leu	Pro	Gly	Phe	His	Met	Leu	Thr	Asp	Ala	Gly	Cys	
					115					120				125		
acc	caa	gac	cag	aga	ctg	cta	gac	tcc	aag	tgt	gac	tgt	gac	cca	gct	549
Thr	Gln	Asp	Gln	Arg	Leu	Leu	Asp	Ser	Lys	Cys	Asp	Cys	Asp	Pro	Ala	
					130					135				140		
ggc	atc	gca	ggg	ccc	tgt	gac	gcf	ggc	cgc	tgt	gtc	tgc	aag	cca	gct	597
Gly	Ile	Ala	Gly	Pro	Cys	Asp	Ala	Gly	Arg	Cys	Val	Cys	Lys	Pro	Ala	
					145					150				155		
gtt	act	gga	gaa	cgc	tgt	gat	agg	tgt	cga	tca	ggf	tac	tat	aat	ctg	645
Val	Thr	Gly	Glu	Arg	Cys	Asp	Arg	Cys	Arg	Ser	Gly	Tyr	Tyr	Asn	Leu	
					165					170				175		
gat	ggg	ggg	aac	cct	gag	ggc	tgt	acc	cag	tgt	ttc	tgc	tat	ggg	cat	693
Asp	Gly	Gly	Asn	Pro	Glu	Gly	Cys	Thr	Gln	Cys	Phe	Cys	Tyr	Gly	His	
					180					185				190		
tca	gcc	agc	tgc	cgc	agc	tct	gca	gaa	tac	agt	gtc	cat	aag	atc	acc	741
Ser	Ala	Ser	Cys	Arg	Ser	Ser	Ala	Glu	Tyr	Ser	Val	His	Lys	Ile	Thr	
					195					200				205		
tct	acc	ttt	cat	caa	gat	gtt	gat	ggc	tgg	aag	gct	gtc	caa	cga	aat	789
Ser	Thr	Phe	His	Gln	Asp	Val	Asp	Gly	Trp	Lys	Ala	Val	Gln	Arg	Asn	
					210					215				220		
ggg	tct	cct	gca	aag	ctc	caa	tgg	tca	cag	cgc	cat	caa	gat	gtg	ttt	837
Gly	Ser	Pro	Ala	Lys	Leu	Gln	Trp	Ser	Gln	Arg	His	Gln	Asp	Val	Phe	
					225					230				235		
240																
agc	tca	gcc	caa	cga	cta	gat	cct	gtc	tat	ttt	gtg	gct	cct	gcc	aaa	885
Ser	Ser	Ala	Gln	Arg	Leu	Asp	Pro	Val	Tyr	Phe	Val	Ala	Pro	Ala	Lys	
					245					250				255		
ttt	ctt	ggg	aat	caa	cag	gtg	agc	tat	ggg	caa	agc	ctg	tcc	ttt	gac	933
Phe	Leu	Gly	Asn	Gln	Gln	Val	Ser	Tyr	Gly	Gln	Ser	Leu	Ser	Phe	Asp	
					260					265				270		
tac	cgt	gtg	gac	aga	gga	ggc	aga	cac	cca	tct	gcc	cat	gat	gtg	atc	981
Tyr	Arg	Val	Asp	Arg	Gly	Gly	Arg	His	Pro	Ser	Ala	His	Asp	Val	Ile	
					275					280				285		
ctg	gaa	ggf	gct	ggf	cta	cgf	atc	aca	gct	ccc	ttg	atg	cca	ctt	ggc	1029
Leu	Glu	Gly	Ala	Gly	Leu	Arg	Ile	Thr	Ala	Pro	Leu	Met	Pro	Leu	Gly	

290	295	300	
aag aca ctg cct tgt ggg ctc acc aag act tac aca ttc agg tta aat Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn 305 310 315 320			1077
gag cat cca agc aat aat tgg agc ccc cag ctg agt tac ttt gag tat Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr 325 330 335			1125
cga agg tta ctg cgg aat ctc aca gcc ctc cgc atc cga gct aca tat Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr 340 345 350			1173
gga gaa tac agt act ggg tac att gac aat gtg acc ctg att tca gcc Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala 355 360 365			1221
cgc cct gtc tct gga gcc cca gca ccc tgg gtt gaa cag tgt ata tgt Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys 370 375 380			1269
cct gtt ggg tac aag ggg caa ttc tgc cag gat tgt gct tct ggc tac Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr 385 390 395 400			1317
aag aga gat tca gcg aga ctg ggg cct ttt ggc acc tgt att cct tgt Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys 405 410 415			1365
aac tgt caa ggg gga ggg gcc tgt gat cca gac aca gga gat tgt tat Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr 420 425 430			1413
tca ggg gat gag aat cct gac att gag tgt gct gac tgc cca att ggt Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly 435 440 445			1461
ttc tac aac gat ccg cac gac ccc cgc agc tgc aag cca tgt ccc tgt Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys 450 455 460			1509
cat aac ggg ttc agc tgc tca gtg att ccg gag acg gag gag gtg gtg His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val 465 470 475 480			1557
tgc aat aac tgc cct ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys 485 490 495			1605
gct gat ggc tac ttt ggg gac ccc ttt ggt gaa cat ggc cca gtg agg Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg 500 505 510			1653
cct tgt cag ccc tgt caa tgc aac agc aat gtg gac ccc agt gcc tct Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser 515 520 525			1701

ggg aat tgt gac cgg ctg aca ggc agg tgt ttg aag tgt atc cac aac Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn	1749
530 535 540	
aca gcc ggc atc tac tgc gac cag tgc aaa gca ggc tac ttc ggg gac Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp	1797
545 550 555 560	
cca ttg gct ccc aac cca gca gac aag tgt cga gct tgc aac tgt aac Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn	1845
565 570 575	
ccc atg ggc tca gag cct gta gga tgt cga agt gat ggc acc tgt gtt Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val	1893
580 585 590	
tgc aag cca gga ttt ggt ggc ccc aac tgt gag cat gga gca ttc agc Cys Lys Pro Gly Phe Gly Pro Asn Cys Glu His Gly Ala Phe Ser	1941
595 600 605	
tgt cca gct tgc tat aat caa gtg aag att cag atg gat cag ttt atg Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met	1989
610 615 620	
cag cag ctt cag aga atg gag gcc ctg att tca aag gct cag ggt ggt Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly	2037
625 630 635 640	
gat gga gta gta cct gat aca gag ctg gaa ggc agg atg cag cag gct Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala	2085
645 650 655	
gag cag gcc ctt cag gac att ctg aga gat gcc cag att tca gaa ggt Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly	2133
660 665 670	
gct agc aga tcc ctt ggt ctc cag ttg gcc aag gtg agg agc caa gag Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu	2181
675 680 685	
aac agc tac cag agc cgc ctg gat gac ctc aag atg act gtg gaa aga Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg	2229
690 695 700	
gtt cggt gct ctg gga agt cag tac cag aac cga gtt cggt gat act cac Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His	2277
705 710 715 720	
agg ctc atc act cag atg cag ctg agc ctg gca gaa agt gaa gct tcc Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser	2325
725 730 735	
ttg gga aac act aac att cct gcc tca gac cac tac gtg ggg cca aat Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn	2373
740 745 750	

ggc ttt aaa agt ctg gct cag gag gcc aca aga tta gca gaa agc cac		2421	
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His			
755	760	765	
gtt gag tca gcc agt aac atg gag caa ctg aca agg gaa act gag gac		2469	
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp			
770	775	780	
tat tcc aaa caa gcc ctc tca ctg gtg cgcc aag gac ctg cat gaa gga		2517	
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly			
785	790	795	800
gtc gga agc gga agc ggt agc ccg gac ggt gct gtg gtg caa ggg ctt		2565	
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu			
805	810	815	
gtg gaa aaa ttg gag aaa acc aag tcc ctg gcc cag cag ttg aca agg		2613	
Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg			
820	825	830	
gag gcc act caa gcg gaa att gaa gca gat agg tct tat cag cac agt		2661	
Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser			
835	840	845	
ctc cgc ctc ctg gat tca gtg tct ccg ctt cag gga gtc agt gat cag		2709	
Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln			
850	855	860	
tcc ttt cag gtg gaa gaa gca aag agg atc aaa caa aaa gcg gat tca		2757	
Ser Phe Gln Val Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser			
865	870	875	880
ctc tca agc ctg gta acc agg cat atg gat gag ttc aag cgt aca caa		2805	
Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln			
885	890	895	
aag aat ctg gga aac tgg aaa gaa gaa gca cag cag ctc tta cag aat		2853	
Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn			
900	905	910	
gga aaa agt ggg aga gag aaa tca gat cag ctg ctt tcc cgt gcc aat		2901	
Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn			
915	920	925	
ctt gct aaa agc aga gca caa gaa gca ctg agt atg ggc aat gcc act		2949	
Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr			
930	935	940	
ttt tat gaa gtt gag agc atc ctt aaa aac ctc aga gag ttt gac ctg		2997	
Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu			
945	950	955	960
cag gtg gac aac aga aaa gca gaa gct gaa gaa gcc atg aag aga ctc		3045	
Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu			
965	970	975	
tcc tac atc agc cag aag gtt tca gat gcc agt gac aag acc cag caa		3093	

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
 980 985 990
 gca gaa aga gcc ctg ggg agc gct gct gct gat gca cag agg gca aag 3141
 Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
 995 1000 1005
 aat ggg gcc ggg gag gcc ctg gaa atc tcc agt gag att gaa cag 3186
 Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
 1010 1015 1020
 gag att ggg agt ctg aac ttg gaa gcc aat gtg aca gca gat gga 3231
 Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
 1025 1030 1035
 gcc ttg gcc atg gaa aag gga ctg gcc tct ctg aag agt gag atg 3276
 Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
 1040 1045 1050
 agg gaa gtg gaa gga gag ctg gaa agg aag gag ctg gag ttt gac 3321
 Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
 1055 1060 1065
 acg aat atg gat gca gta cag atg gtg att aca gaa gcc cag aag 3366
 Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
 1070 1075 1080
 gtt gat acc aga gcc aag aac gct ggg gtt aca atc caa gac aca 3411
 Val Asp Thr Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr
 1085 1090 1095
 ctc aac aca tta gac ggc ctc ctg cat ctg atg gac cag cct ctc 3456
 Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met Asp Gln Pro Leu
 1100 1105 1110
 agt gta gat gaa gag ggg ctg gtc tta ctg gag cag aag ctt tcc 3501
 Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln Lys Leu Ser
 1115 1120 1125
 cga gcc aag acc cag atc aac agc caa ctg cg^g ccc atg atg tca 3546
 Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met Met Ser
 1130 1135 1140
 gag ctg gaa gag agg gca cgt cag cag agg ggc cac ctc cat ttg 3591
 Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His Leu
 1145 1150 1155
 ctg gag aca agc ata gat ggg att ctg gct gat gtg aag aac ttg 3636
 Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu
 1160 1165 1170
 gag aac att agg gac aac ctg ccc cca ggc tgc tac aat acc cag 3681
 Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln
 1175 1180 1185
 gct ctt gag caa cag tga agctgccata aatatttctc aactgagggt 3729
 Ala Leu Glu Gln Gln

1190

cttggatac agatctcagg gctcgggagc catgtcatgt gagtggtgg gatgggaca	3789
ttaaatgggt atgctcaggt caactgacct gacccattc ctgatccat	3849
ggccaggtgg ttgtcttatt gcaccatact cttgcttcc ttagtgcgtgg catgaggcag	3909
ataggcactg gtgtgagaat gatcaaggat ctggaccca aagatagact ggatggaaag	3969
acaactgca caggcagatg tttgcctcat aatagtcgt aatggagtc tggaatttgg	4029
acaagtgctg ttggatata gtcaacttat tcatttgcgtt atgtgactaa aggaaaaaac	4089
tttgcatttgc cccaggcatg aaattcttcc taatgtcaga acagagtgc acccagtcac	4149
actgtggcca gtaaaaactt attgcctcat attgtcctct gcaagcttct tgctgatcag	4209
atccctcct acttacaacc cagggtgtga acatgttctc cattttcaag ctggagaag	4269
tgagcagtgt tggagtgagg acctgttgcgtt caggccattt cagagctatg gtgcatttgc	4329
gtgcctgcca ctttcaagtt ctggacctgg gcatgacatc ctttcttta atgtgccat	4389
ggcaacttag agattgcatt ttattaaag catttcctac cagcaaagca aatgtggga	4449
aagtatttac ttttcgggtt tcaaagtgtt agaaaagtgt ggcttggca ttgaaagagg	4509
taaaattctc tagatttatt agtcctaatt caatcctact ttcaacac caaaaatgt	4569
gcgcataat gtattttatc ttattttctc aatctcctct ctcttcctc caccataat	4629
aagagaatgt tcctactcac acttcagctg ggtcacatcc atccctccat tcatttcctc	4689
atccatctt ccatccatta cctccatcca tccttccaaat atatattt tgatgttac	4749
ctgtgtgcca ggggctgggtt ggacagtggt gacatgtct ctgcctcat agagttgatt	4809
gtcttagttagt gaagacaagc atttttaaaa aataaattt aacttacaaa ctttgttgc	4869
cacaagtggt gtttatttgcata acccgctt ggttgcaac ctcttcgtt aacagaacat	4929
atgttgcag accctccat gggactgag tttggcaagg atgacagagc tctgggttgc	4989
gcacatttctt ttgcattcca gctcactctt gtgccttcta caactgatttgc caacagactg	5049
tttagttatgtt ataacaccat tggaaatttgc tggaggaacc agaggcattt ccacccggc	5109
tggaaagact atgggtgtgc ctgcatttgc tatttccttgc gatggatgttgc aaagtgtttt	5169
taaataaaga acaattgtt aatgtccaaa a	5200

<210> 2
<211> 1193
<212> PRT
<213> Homo sapiens

<400> 2

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
1 5 10 15

Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
20 25 30

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
35 40 45

Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
50 55 60

Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
65 70 75 80

Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
85 90 95

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
100 105 110

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
115 120 125

Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
130 135 140

Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145 150 155 160

Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
165 170 175

Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
180 185 190

Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
195 200 205

Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
210 215 220

Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225 230 235 240

Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
245 250 255

Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
260 265 270

Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
275 280 285

Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
290 295 300

Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305 310 315 320

Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
325 330 335

Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
340 345 350

Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
355 360 365

Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
370 375 380

Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385 390 395 400

Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
405 410 415

Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
420 425 430

Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
435 440 445

Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
450 455 460

His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465 470 475 480

Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
485 490 495

Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
500 505 510

Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
515 520 525

Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
530 535 540

Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545 550 555 560

Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
565 570 575

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
580 585 590

Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
595 600 605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
610 615 620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625 630 635 640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
645 650 655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
660 665 670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
675 680 685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
690 695 700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705 710 715 720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
725 730 735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
740 745 750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
755 760 765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
770 775 780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
 785 790 795 800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
805 810 815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
820 825 830

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
835 840 845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
850 855 860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865 870 875 880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
885 890 895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn

900

905

910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
915 920 925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
930 935 940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945 950 955 960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
965 970 975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
980 985 990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
995 1000 1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
1010 1015 1020

Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
1025 1030 1035

Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
1040 1045 1050

Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
1055 1060 1065

Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
1070 1075 1080

Val Asp Thr Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr
1085 1090 1095

Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met Asp Gln Pro Leu
1100 1105 1110

Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln Lys Leu Ser
1115 1120 1125

Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met Met Ser
1130 1135 1140

Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His Leu
1145 1150 1155

Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu
1160 1165 1170

Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln
1175 1180 1185

Ala Leu Glu Gln Gln
1190

<210> 3
<211> 4316
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> (118)..(183)
<223>

<220>
<221> CDS
<222> (118)..(3453)
<223>

<220>
<221> repeat_unit
<222> (4021)..(4316)
<223>

<220>
<221> polyA_site
<222> (4296)..(4316)
<223>

<400> 3
gaccacctga tcgaaggaaa aggaaggcac agcggagcgc agagtgagaa ccaccaaccg 60

aggcgccggg cagcgacccc tgcagcggag acagagactg agcggcccg caccgcc 117

atg cct gcg ctc tgg ctg ggc tgc tgc ctc tgc ttc tgc ctc ctc ctg 165
Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
1 5 10 15

ccc gca gcc cggtt gcc acc tcc agg agg gaa gtc tgt gat tgc aat ggg 213

Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly			
20	25	30	
aag tcc agg cag tgt atc ttt gat cgg gaa ctt cac aga caa act ggt			261
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly			
35	40	45	
aat gga ttc cgc tgc ctc aac tgc aat gac aac act gat ggc att cac			309
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His			
50	55	60	
tgc gag aag tgc aag aat ggc ttt tac cgg cac aga gaa agg gac cgc			357
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg			
65	70	75	80
tgt ttg ccc tgc aat tgt aac tcc aaa ggt tct ctt agt gct cga tgt			405
Cys Leu Pro Cys Asn Cys Ser Lys Gly Ser Leu Ser Ala Arg Cys			
85	90	95	
gac aac tct gga cgg tgc agc tgt aaa cca ggt gtg aca gga gcc aga			453
Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg			
100	105	110	
tgc gac cga tgt ctg cca ggc ttc cac atg ctc acg gat gcg ggg tgc			501
Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys			
115	120	125	
acc caa gac cag aga ctg cta gac tcc aag tgt gac tgt gac cca gct			549
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala			
130	135	140	
ggc atc gca ggg ccc tgt gac gcg ggc cgc tgt gtc tgc aag cca gct			597
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala			
145	150	155	160
gtt act gga gaa cgc tgt gat agg tgt cga tca ggt tac tat aat ctg			645
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu			
165	170	175	
gat ggg ggg aac cct gag ggc tgt acc cag tgt ttc tgc tat ggg cat			693
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His			
180	185	190	
tca gcc agc tgc cgc agc tct gca gaa tac agt gtc cat aag atc acc			741
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr			
195	200	205	
tct acc ttt cat caa gat gtt gat ggc tgg aag gct gtc caa cga aat			789
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn			
210	215	220	
ggg tct cct gca aag ctc caa tgg tca cag cgc cat caa gat gtg ttt			837
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe			
225	230	235	240
agc tca gcc caa cga cta gat cct gtc tat ttt gtg gct cct gcc aaa			885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys			

245	250	255	
ttt ctt ggg aat caa cag gtg agc tat ggg caa agc ctg tcc ttt gac Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp	260	265	933
tac cgt gtg gac aga gga ggc aga cac cca tct gcc cat gat gtg atc Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile	275	280	981
ctg gaa ggt gct ggt cta cg ^g atc aca gct ccc ttg atg cca ctt ggc Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly	290	295	1029
aag aca ctg cct tgt ggg ctc acc aag act tac aca ttc agg tta aat Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn	305	310	1077
gag cat cca agc aat aat tgg agc ccc cag ctg agt tac ttt gag tat Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr	325	330	1125
cga agg tta ctg cgg aat ctc aca gcc ctc cgc atc cga gct aca tat Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr	340	345	1173
gga gaa tac agt act ggg tac att gac aat gtg acc ctg att tca gcc Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala	355	360	1221
cgc cct gtc tct gga gcc cca gca ccc tgg gtt gaa cag tgt ata tgt Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys	370	375	1269
cct gtt ggg tac aag ggg caa ttc tgc cag gat tgt gct tct ggc tac Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr	385	390	1317
395	400		
aag aga gat tca gc ^g aga ctg ggg cct ttt ggc acc tgt att cct tgt Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys	405	410	1365
415			
aac tgt caa ggg gga ggg gcc tgt gat cca gac aca gga gat tgt tat Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr	420	425	1413
430	435		
tca ggg gat gag aat cct gac att gag tgt gct gac tgc cca att ggt Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly	440	445	1461
450	455	460	
ttc tac aac gat ccg cac gac ccc cgc agc tgc aag cca tgt ccc tgt Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys	470	475	1509
480			
cat aac ggg ttc agc tgc tca gtg att ccg gag acg gag gag gtg gtg His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val	495	500	1557

tgc aat aac tgc cct ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys 485 490 495	1605
gct gat ggc tac ttt ggg gac ccc ttt ggt gaa cat ggc cca gtg agg Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg 500 505 510	1653
cct tgt cag ccc tgt caa tgc aac agc aat gtg gac ccc agt gcc tct Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser 515 520 525	1701
ggg aat tgt gac cg ^g ctg aca ggc agg tgt ttg aag tgt atc cac aac Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn 530 535 540	1749
aca gcc ggc atc tac tgc gac cag tgc aaa gca ggc tac ttc ggg gac Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp 545 550 555 560	1797
cca ttg gct ccc aac cca gca gac aag tgt cga gct tgc aac tgt aac Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn 565 570 575	1845
ccc atg ggc tca gag cct gta gga tgt cga agt gat ggc acc tgt gtt Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val 580 585 590	1893
tgc aag cca gga ttt ggt ggc ccc aac tgt gag cat gga gca ttc agc Cys Lys Pro Gly Phe Gly Pro Asn Cys Glu His Gly Ala Phe Ser 595 600 605	1941
tgt cca gct tgc tat aat caa gtg aag att cag atg gat cag ttt atg Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met 610 615 620	1989
cag cag ctt cag aga atg gag gcc ctg att tca aag gct cag ggt ggt Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly 625 630 635 640	2037
gat gga gta gta cct gat aca gag ctg gaa ggc agg atg cag cag gct Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala 645 650 655	2085
gag cag gcc ctt cag gac att ctg aga gat gcc cag att tca gaa ggt Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly 660 665 670	2133
gct agc aga tcc ctt ggt ctc cag ttg gcc aag gtg agg agc caa gag Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu 675 680 685	2181
aac agc tac cag agc cgc ctg gat gac ctc aag atg act gtg gaa aga Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg 690 695 700	2229

gtt	cgg	gct	ctg	gga	agt	cag	tac	cag	aac	cga	gtt	cgg	gat	act	cac		2277
Val	Arg	Ala	Leu	Gly	Ser	Gln	Tyr	Gln	Asn	Arg	Val	Arg	Asp	Thr	His		
705							710			715					720		
agg	ctc	atc	act	cag	atg	cag	ctg	agc	ctg	gca	gaa	agt	gaa	gct	tcc		2325
Arg	Leu	Ile	Thr	Gln	Met	Gln	Leu	Ser	Leu	Ala	Glu	Ser	Glu	Ala	Ser		
							725			730					735		
ttg	gga	aac	act	aac	att	cct	gcc	tca	gac	cac	tac	gtg	ggg	cca	aat		2373
Leu	Gly	Asn	Thr	Asn	Ile	Pro	Ala	Ser	Asp	His	Tyr	Val	Gly	Pro	Asn		
							740			745					750		
ggc	ttt	aaa	agt	ctg	gct	cag	gag	gcc	aca	aga	tta	gca	gaa	agc	cac		2421
Gly	Phe	Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Leu	Ala	Glu	Ser	His		
							755			760					765		
gtt	gag	tca	gcc	agt	aac	atg	gag	caa	ctg	aca	agg	gaa	act	gag	gac		2469
Val	Glu	Ser	Ala	Ser	Asn	Met	Glu	Gln	Leu	Thr	Arg	Glu	Thr	Glu	Asp		
							770			775					780		
tat	tcc	aaa	caa	gcc	ctc	tca	ctg	gtg	cgc	aag	gcc	ctg	cat	gaa	gga		2517
Tyr	Ser	Lys	Gln	Ala	Leu	Ser	Leu	Val	Arg	Lys	Ala	Leu	His	Glu	Gly		
							785			790					795		800
gtc	gga	agc	gga	agc	ggt	agc	ccg	gac	ggt	gct	gtg	gtg	caa	ggg	ctt		2565
Val	Gly	Ser	Gly	Ser	Gly	Ser	Pro	Asp	Gly	Ala	Val	Val	Gln	Gly	Leu		
							805			810					815		
gtg	gaa	aaa	ttg	gag	aaa	acc	aag	tcc	ctg	gcc	cag	cag	ttg	aca	agg		2613
Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg		
							820			825					830		
gag	gcc	act	caa	gcg	gaa	att	gaa	gca	gat	agg	tct	tat	cag	cac	agt		2661
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser		
							835			840					845		
ctc	cgc	ctc	ctg	gat	tca	gtg	tct	ccg	ctt	cag	gga	gtc	agt	gat	cag		2709
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Pro	Leu	Gln	Gly	Val	Ser	Asp	Gln		
							850			855					860		
tcc	ttt	cag	gtg	gaa	gaa	gca	aag	agg	atc	aaa	caa	aaa	gcg	gat	tca		2757
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser		
							865			870					875		880
ctc	tca	agc	ctg	gta	acc	agg	cat	atg	gat	gag	ttc	aag	cgt	aca	caa		2805
Leu	Ser	Ser	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln		
							885			890					895		
aag	aat	ctg	gga	aac	tgg	aaa	gaa	gaa	gca	cag	cag	ctc	tta	cag	aat		2853
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn		
							900			905					910		
gga	aaa	agt	ggg	aga	gag	aaa	tca	gat	cag	ctg	ctt	tcc	cgt	gcc	aat		2901
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn		
							915			920					925		
ctt	gct	aaa	agc	aga	gca	caa	gaa	gca	ctg	agt	atg	ggc	aat	gcc	act		2949

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr			
930	935	940	
ttt tat gaa gtt gag agc atc ctt aaa aac ctc aga gag ttt gac ctg			2997
Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu			
945	950	955	960
cag gtg gac aac aga aaa gca gaa gct gaa gaa gcc atg aag aga ctc			3045
Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu			
965	970	975	
tcc tac atc agc cag aag gtt tca gat gcc agt gac aag acc cag caa			3093
Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln			
980	985	990	
gca gaa aga gcc ctg ggg agc gct gct gct gat gca cag agg gca aag			3141
Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys			
995	1000	1005	
aat ggg gcc ggg gag gcc ctg gaa atc tcc agt gag att gaa cag			3186
Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln			
1010	1015	1020	
gag att ggg agt ctg aac ttg gaa gcc aat gtg aca gca gat gga			3231
Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly			
1025	1030	1035	
gcc ttg gcc atg gaa aag gga ctg gcc tct ctg aag agt gag atg			3276
Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met			
1040	1045	1050	
agg gaa gtg gaa gga gag ctg gaa agg aag gag ctg gag ttt gac			3321
Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp			
1055	1060	1065	
acg aat atg gat gca gta cag atg gtg att aca gaa gcc cag aag			3366
Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys			
1070	1075	1080	
gtt gat acc aga gcc aag aac gct ggg gtt aca atc caa gac aca			3411
Val Asp Thr Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr			
1085	1090	1095	
ctc aac aca tta gac ggc ctc ctg cat ctg atg ggt atg tga			3453
Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met Gly Met			
1100	1105	1110	
acccacaacc cacaacccatc cagctccatg ctccagggt ttgctccaga acactca			3513
tacctagccc cagcaaaggg gagtctcagc ttcccttaag gatatcagta aatgtgottt			3573
gtttccaggc ccagataact ttccggcaggc tcccttacat ttactggacc ctgtttacc			3633
gttgctaaga tgggtcactg aacacctatt gcacttgggg gtaaaggct gtggggccaaa			3693
gaacagggtgt atataagcaa cttcacagaa cacgagacag cttgggaatc ctgctaaaga			3753

gtctggcctg	gaccctgaga	agccagtgga	cagtttaag	cagaggaata	acatcaccac	3813
tgtatatttc	agaaagatca	ctagggcagc	cgagtggagg	aaagcttcaa	gagggggta	3873
gagagaaggc	aggttgagac	tacttaagat	attgtgaaa	taattgaaga	gagaaatgac	3933
aggagcctgc	tctaaggcag	tagaatggtg	gctggaaaga	tgtgaaggaa	gatttccca	3993
gtctgtgaag	tcaagaatca	cttgccggcc	gggtgtggtg	gctcacgcct	gtaattctag	4053
cacttggaa	gactgaagcg	ggtggatcac	ccgaggtcag	gagttgaaga	ccagcctggc	4113
caacatggtg	aaaccctgtc	tctactaaaa	gtacaaaaat	tagctggatg	atggtgtgg	4173
gcgcctgtaa	ttccagctac	tcaggagtct	gaggcaggag	aatcgcttga	acccaggagg	4233
cgaggttaca	gtgagccaag	attgcaccac	tgctcttcca	gcctggaaac	agagagactg	4293
cctaaaaaaaaa	aaaaaaaaaa	aaaaaaa	aaa			4316

<210> 4
 <211> 1111
 <212> PRT
 <213> Homo sapiens

<400> 4

Met	Pro	Ala	Leu	Trp	Leu	Gly	Cys	Cys	Leu	Cys	Phe	Ser	Leu	Leu	Leu
1				5					10					15	

Pro	Ala	Ala	Arg	Ala	Thr	Ser	Arg	Arg	Glu	Val	Cys	Asp	Cys	Asn	Gly
				20					25					30	

Lys	Ser	Arg	Gln	Cys	Ile	Phe	Asp	Arg	Glu	Leu	His	Arg	Gln	Thr	Gly
				35					40					45	

Asn	Gly	Phe	Arg	Cys	Leu	Asn	Cys	Asn	Asp	Asn	Thr	Asp	Gly	Ile	His
				50					55					60	

Cys	Glu	Lys	Cys	Lys	Asn	Gly	Phe	Tyr	Arg	His	Arg	Glu	Arg	Asp	Arg
				65					70					75	80

Cys	Leu	Pro	Cys	Asn	Cys	Asn	Ser	Lys	Gly	Ser	Leu	Ser	Ala	Arg	Cys
				85					90					95	

Asp	Asn	Ser	Gly	Arg	Cys	Ser	Cys	Lys	Pro	Gly	Val	Thr	Gly	Ala	Arg
				100					105					110	

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys

	115	120	125
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala			
130	135	140	
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala			
145	150	155	160
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu			
165	170	175	
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His			
180	185	190	
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr			
195	200	205	
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn			
210	215	220	
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe			
225	230	235	240
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys			
245	250	255	
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp			
260	265	270	
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile			
275	280	285	
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly			
290	295	300	
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn .			
305	310	315	320
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr			
325	330	335	
Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr			
340	345	350	

Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
355 360 365

Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
370 375 380

Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385 390 395 400

Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
405 410 415

Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
420 425 430

Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
435 440 445

Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
450 455 460

His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465 470 475 480

Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
485 490 495

Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
500 505 510

Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
515 520 525

Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
530 535 540

Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545 550 555 560

Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
565 570 575

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
580 585 590

Cys Lys Pro Gly Phe Gly Pro Asn Cys Glu His Gly Ala Phe Ser
595 600 605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
610 615 620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625 630 635 640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
645 650 655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
660 665 670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
675 680 685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
690 695 700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705 710 715 720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
725 730 735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
740 745 750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
755 760 765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
770 775 780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785 790 795 800

Val Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
805 810 815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
820 825 830

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
835 840 845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
850 855 860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865 870 875 880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
885 890 895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
900 905 910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
915 920 925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
930 935 940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945 950 955 960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
965 970 975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
980 985 990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
995 1000 1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
1010 1015 1020

Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly

1025 1030 1035
Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
1040 1045 1050

Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
1055 1060 1065

Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
1070 1075 1080

Val Asp Thr Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr
1085 1090 1095

Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met Gly Met
1100 1105 1110

.
<210> 5
<211> 530
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Portion of Domain III of laminin gamma 2

<400> 5
aattctgcca ggatttgct tctggctaca agagagattc agcgagactg gggcctttg 60
gcacctgtat tccttgtaac tgtcaagggg gaggggcctg tgatccagac acaggagatt 120
gttattcagg gnatgagaat cctgacattt agtgtgctga ctgcccatt gtttctaca 180
acgatccgca cgacccccgc agctgcaagc catgtccctg tcataacggg ttcagctgct 240
cagtgattcc ggagacggag gaggtggtgt gcaataactg ccctcccggt gtcaccgggt 300
cccgctgtga gctctgtct gatggctact ttggggaccc ctttggtgaa catggccca 360
tgaggcatttgc tcaagccctgt caatgcaaca gcaatgtgga ccccagtgcc tctggaaatt 420
gtgaccggct gacaggcagg tggtaagt gtatccacaa cacagccggc atctactgct 480
accagtgcaa agcaggctac ttccgggacc cattggctcc caacccagca 530

<210> 6
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Portion of Domain III of laminin gamma 2.

<400> 6

Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala Arg
1 5 10 15

Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly Gly
20 25 30

Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn Pro
35 40 45

Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro His
50 55 60

Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser Cys
65 70 75 80

Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro Pro
85 90 95

Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly
100 105 110

Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys Gln
115 120 125

Cys Asn Asn Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg Leu
130 135 140

Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr Cys
145 150 155 160

Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn Pro
165 170 175

Ala

<210> 7

<211> 681
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Complete domain III of laminin gamma 2

<400> 7
tgtatatgtc ctgttggta caagggcaa ttctgccagg atttgcttc tggctacaag 60
agagattcag cgagactggg gcctttggc acctgtattc cttgttaactg tcaagggga 120
ggggcctgtg atccagacac aggagattgt tattcagggg atgagaatcc tgacatttag 180
tgtgctgact gccaaattgg tttctacaac gatccgcacg acccccgcag ctgcaagcca 240
tgtccctgtc ataacgggtt cagctgctca gtgattccgg agacggagga ggtggtgtgc 300
aataactgcc ctccccgggtt caccgggtgcc cgctgtgagc tctgtgctga tggctacttt 360
ggggacccct ttggtaaca tggcccagtgc aggccttgtc agccctgtca atgcaacagc 420
aatgtggacc ccagtgcctc tggaaattgt gaccggctga caggcaggtg tttgaagtgt 480
atccacaaca cagccggcat ctactgcgac cagtcaaaag caggctactt cggggaccca 540
ttggctccca acccagcaga caagtgtcga gcttgcact gtaacccat gggctcagag 600
cctgttaggat gtcgaagtga tggcacctgt gtttgcagc caggatttg tggccccaac 660
tgtgagcatg gagcattcag c 681

<210> 8
<211> 227
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Complete domain III of laminin gamma 2.

<400> 8
Cys Ile Cys Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala
1 5 10 15

Ser Gly Tyr Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys
20 25 30

Ile Pro Cys Asn Cys Gln Gly Gly Ala Cys Asp Pro Asp Thr Gly
35 40 45

Asp Cys Tyr Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys
50 55 60

Pro Ile Gly Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro
65 70 75 80

Cys Pro Cys His Asn Gly Phe Ser Cys Ser Val Met Pro Glu Thr Glu
85 90 95

Glu Val Val Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys
100 105 110

Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly
115 120 125

Pro Val Arg Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn Val Asp Pro
130 135 140

Ser Ala Ser Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys
145 150 155 160

Ile His Asn Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr
165 170 175

Phe Gly Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys
180 185 190

Asn Cys Asn Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly
195 200 205

Thr Cys Val Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly
210 215 220

Ala Phe Ser
225

<210> 9
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature

<223> N-terminal portion of domain III of laminin gamma 2.

<400> 9

Cys Ile Cys Pro Val Gly Tyr Lys Gly
1 5

<210> 10

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> C-terminal portion of domain III of laminin gamma 2.

<400> 10

Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu Pro Val
1 5 10 15

Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe Gly Gly
20 25 30

Pro Asn Cys Glu His Gly Ala Phe Ser
35 40

1